

Amendments to the Claims:

This listing of claims will replace all prior versions, and listings of claims in the application:

Listing of Claims:

Claim 1. (Previously Presented) A method of detecting cancer in a patient, the method comprising the steps of:

- (i) determining the level of a transcript encoding SEQ ID NO:2 in a biological sample from the patient; and
 - (ii) detecting a decrease in the level of the transcript relative to normal, thereby detecting the presence of cancer in the patient;
- wherein the cancer is characterized by having a methylation of a SOCS-3 promoter.

Claim 2. (Original) The method of claim 1, wherein the cancer is selected from a group consisting of lung cancer, breast cancer, mesothelioma, colon cancer, and sarcoma.

Claim 3. (Original) The method of claim 1, wherein the step of determining the level of the transcript comprises an amplification reaction.

Claims 4-11. (Cancelled)

Claim 12. (Original) A method of monitoring the efficacy of a therapeutic treatment of cancer, the method comprising the steps of:

- (i) providing a biological sample from a patient undergoing the therapeutic treatment; and
- (ii) detecting the level of: a polypeptide having an amino acid sequence of SEQ ID NO:2, or of a nucleic acid that encodes the polypeptide, in the biological sample compared to a level in a biological sample from the patient prior to, or earlier in, the therapeutic treatment, thereby monitoring the efficacy of the therapy.

Claims 13-25. (Cancelled)

Claim 26. (Previously Presented) The method of claim 1, wherein the step of determining the level of the transcript comprises a nucleic acid hybridization assay.

Claim 27. (Previously Presented) The method of claim 26, wherein the nucleic acid hybridization assay is selected from the group consisting of Northern blot, dot blotting, in situ hybridization, RNase protection, and probing a DNA microchip array.

Claim 28. (Previously Presented) The method of claim 1, wherein the transcript comprises SEQ ID NO:1.

Claim 29. (Previously Presented) The method of claim 3, wherein the amplification reaction is selected from the group consisting of polymerase chain reaction, quantitative polymerase chain reaction, ligase chain reaction, transcription amplification, self-sustained sequence replication, dot polymerase chain reaction, and linker adapter polymerase chain reaction.

Claim 30. (Previously Presented) The method of claim 3, wherein the amplification reaction comprises SEQ ID NO:9 and SEQ ID NO:10.

Claim 31. (Previously Presented) The method of claim 1, wherein the methylation of the SOCS-3 promoter occurs within the region from -1005 to -983 or from -754 to -737 of SEQ ID NO:3.